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Listing first 45 summaries
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Ig kappa chain - m monoclonal antibod Ig kappa chain V r Ig kappa chain I v r Ig kappa chain - m Ig kappa chain (Mono Ig kappa chain V r Ig kappa chain V r Ig kappa chain I NIG Ig kappa chain I NIG Ig kappa chain NIG Ig kappa chain NIG Ig kappa chain I V r Ig kappa chain I I V r Ig kappa chain I V r Ig Kappa
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            A; Molecule type: protein
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RESULT JC5810 monoclona C; Species C; Date: C; Accessi R; Akashi Biochem A; Title: A; Referer A; Recessi	OY OY OY OY	Qu Be Ma Qy Db	RESU S250 C; Sp C; Sp C; Sp C; A C; A S; Dbn A; Ree A; Ree A; Re A; Re C; Su C; Su		
RESULT 2 JC5910 monoclonal a C; species: M C; Date: 04-F; C; Accession: C; Accession: B; Accession: B; Accession: A; Reference A; Reference A; Reference	63 83 122 143 182 203	Query M Best Lo Matches	SULT 1 Species: M Species: M Date: 19-M Accession: R bmitted to Descriptio Descriptio Reference Reference Reference Reference Residues: Status: pr Residues: Status: T Residues: Cross-refe Superfamil		00000000000000000000000000000000000000
2 Il anti II anti II anti II Mus II	FSGSG FSGSG FSGSG SEQLT SEQLT TKDEY	atch cal Si 192; VLTQS 	RESULT 1 S25058 Ig kappa chain - mouse C; Species; Mus musculu C; Date: 19-Mar-1997 #s C; Accession: S25058 R; Fischer, R.; Voss, A submitted to the EMBL A; Description: Product A; Description: Product A; Reference number: S2 A; Accession: S25058 A; Sctatus: preliminary A; Molecule type: mRNA A; Residues: 1-235 <fis 38-111="" a;="" c;="" cross·references:="" domain:="" em="" f;="" immunog="" immunog<="" superfamily:="" td=""><td></td><td>4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4</td></fis>		4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
tibody 13-1 s musculus b-1998 #seq JC5810 Kato, K.; hys. Res. C ctural char umber: JC58	SOSGTSYSLTISSWI	milarity 90.1% Conservative PAIMSASPGEKVTMTC			444 444 444 444 444 444 444 444 444 44
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iin - m ise) .sion 1 T.; Do), 566- lon of	GSGTSYSLTISSVEAEDAATTYCQQYSGY	Score 988 pred. No. 6; Mismato 111111 : 1 SASSSVSKMQN	mouse) revision 19-Man bach, M.; Munz; rary, July 199; Tobacco mosai Tobacco mosai 1; NID:954828; V region; immu n homology <immu< td=""><td>ALIGN</td><td>PL0013 JE0246 PT0405 A32513 K1RTA S29577 PT0404 S29575 S04573 S04573 S04573 S04574 S29576 S21066 S21066 S25746 S25746</td></immu<>	ALIGN	PL0013 JE0246 PT0405 A32513 K1RTA S29577 PT0404 S29575 S04573 S04573 S04573 S04574 S29576 S21066 S21066 S25746 S25746
mouse 13-Mar-1998 #text_change 21-Jan-2000 obmae, N.; Yamaguchi, H.; Kamachi, M.; Harada, 572, 1997 mouse monoclonal antibody 13-1 against a porp	PAIMSASPGEKVTMTCRASSSYSSSYLHWYROKSGASPKLWIYSTSNLASGVPAR 62	2.5e-55; 2.5e-55; 2.5e-55; 2.6es 12; Indels 3; Gap YYROKSGASPKLWIYSTSNLASGVPAR 6 :	ouse) vision 19-Mar-1997 #text_change 21-Jan-2000 ch, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F. ry, July 1992 obacco mosaic virus (TMV) inactivating neotop specifi obacco mosaic virus (TMV) inactivating neotop specifi NID:g54828; PIDN:CAA47650.1; PID:g54829 homology <tmm></tmm>	ALIGNMENTS	Ig kappa chain pre Ig lambda chain NI Ig light chain V r Ig kappa chain C r Ig light chain C r Ig light chain - r Ig light chain - r Ig light chain - r Ig light chain r Ig light chain v r Ig light chain pre Ig kappa chain pre Ig kappa chain pre Ig kappa chain V r Ig lambda chain v Ig lambda chain - Ig lambda chain v Ig lambda chain v Ig lambda chain v

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If kappa chain V region (Mabl3-1) - mouse (fragment)
N;Alternate names: immunoglobulin light chain
C;Species: Mus musculus (house mouse)
C;Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ig kappa chain V region (17/9) - mouse C;Species: Mus musculus (house mouse) C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 21-Jan-2000 C;Accession: A31790 R;Schulze-Gahmen, U; Rini, J.M.; Arevalo, J.; Stura, E.A.; Kenten, J.H.; W.J. Biol. Chem. 263, 17100-17105, 1988 A;Reference number: A92686; MUID:89034213 A;Reference number: A92686; MUID:89034213 A;Accession: A31790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-218 <AKA>
C;Comment: This catalytic antibody has peroxidase oxidase. It is
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-94/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                            B
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A; Residues: 1-220 <SCH>
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                                                                                                                                                                                             VLTQSPAIMSASPGEKYTMTCRASSSVSSS---YLHWYRQKSGASPKLWIYSTSNLASGV 59
                                                                                                                                STLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC
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                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
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Pred. No. 6.1e-49;
                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stura, E.A.; Kenten, J.H.; Wilson,
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64

SGSGSGTSYSLTISSVEAEDAATYYCQQYSGYR-TFGGGTKLEIKRADAAPTVSIFPPSS 122

SGSGSGQDYSLTISSLEYEDVGVYYCLRYDEFPFTFGSGTKLEIKRADAAPTVSIFPPSS

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Ig kappa chain precursor (15C5) - mouse C;Species: Mus musculus (house mouse)
C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000 C;Accession: S14237
R;Vandamme, A.M.; Bulens, F.; Bernar, H.; Nelles, L.; Lijnen, R.H.; Collen, Eur. J. Biochem. 192, 767-775, 1990
A;Title: Construction and characterization of a recombinant murine monoclona. A;Reference number: S14236; MUID:91006173
A;Accession: S14237
                                                                                                                                                                             A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-234 <VANN-
A;Cross-references: EMBL:X56394; NID:g51622; PIDN:CAA39805.1; PID:g51623
A;Cross-references: EMBL:X56394; NID:g51622; PIDN:CAA39805.1; PID:g51623
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;36-110/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: nucleic acid sequence
A;Molecule type: mRNA
A;Residues: 'NI',3-212 <TAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphys A;Reference number: S68211; MUID:96085223
A;Accession: S68214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: EMBL: D29670; R; Takagi, M.; Kohda, K.; Hamuro, FEBS Lett. 375, 273-276, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: S68241; S68214
R;Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; submitted to the EMBL Data Library, March 1994
A;Description: Specific peroxidase activity by formation of an a A;Reference number: S68241
A;Accession: S68241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-218 <TAK>
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Best Local Similarity
Matches 172; Conser
                                                                                 Matches
                                                                                                    Query Match
Best Local Similarity
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                       LTQSPAIMSASPGEKVTMTCRASSSVSSSYLHWYRQKSGASPKLWYYSTSNLASGVPARF 63
MTQSPSSMYASLGERVTVTCKASQDI-NSYLSWIQQKPGKSPKTLIYRGNRLVAGVPSRF 82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IFPPSSEQLTSGGASVVCFLNNFYPRDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSMS 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GVPARFSGSGSGTSYSLTISSVEAEDAATYYCQQYSGY-RTFGGGTKLEIKRADAAPTVS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENVLTQSPAIMSASPGEKVTMTCRASSSVSSS---YLHWYRQKSGASPKLWIYSTSNLAS
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                                                                                                    78.28;
79.78;
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78.9%;
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T.; Harada, !
                                                                                 Score 877; DB
Pred. No. 2.3e
l5; Mismatches
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Pred. No. 9.
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.2e-49;
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A.; Yamaguchi, H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            214
                                                                                                                        Length 234
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Ig kappa chain - mouse (fragment)
c;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision
C;Accession: S38865
R;Kipp, B.; Becker, W.; Schlaak, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNĀ
A; Residues: 1-225 <DUC>
A; Residues: 1-225 <DUC>
A; Cross-references: EMBL:X70424; NID:g406254; PIDN:CAA49869.1; PID:g406255
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
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                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-219 <KIP>
                                                                                                                                                                                            submitted to the EMBL Data A; Description: Combination A; Reference number: S38864 A; Accession: S38865
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Ig kappa chain –
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Best Loc
Matches
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;Species: Mus musculus (house mouse)
;Date: 06-Jan-1995 #sequence_revision
                                Query Match
Best Local Similarity
Matches 169; Conser
                                                                                                                 Cross-references: EMBL:227396; NID:g416538; PIDN:CAA81787.1; PID:g416539; Superfamily: immunoglobulin V region; immunoglobulin homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 214
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                                                                                                      heterotetramer; immunoglobulin
                                 Conservative
                                            77.6%;
77.2%;
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79.3%;
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                                16;
                                            Score 869.5; DB 2;
Pred. No. 6.5e-48;
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                                Mismatches
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A;Cross-references: GB:U29147; NID:g1594225; PIDN:AAC52821.1; PID:g1594226
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A; Reference number: PC4202; A; Accession: PC4203
                                                                 R;Kwak, J.W.; Lee, D.I.; Choi, B.K.; Cho, W.K.; Lee, S.H.; Gene 173, 257-259, 1996
A;Title: Cloning and characterization of cDNAs coding for A;Reference number: PC4202; MUID:97082978
                                                                                                                                                                                   Ig kappa chain (monoclonal antibody MabA34) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 11-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:X13187; NID:g51784; PIDN:CAA31579.1; A;Note: this sequence was determined from the differentiated g C;Superfamily: immunoglobulin V region; immunoglobulin homolog C;Keywords: heterotetramer; immunoglobulin immunoglobulin F;1-20/Domain: signal sequence #status predicted <SIG>F;1-20/Domain: Ig kappa chain #status predicted <MAT>F;36-110/Domain: immunoglobulin homology <IMM>
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R;de Waele, P.; Feys,
Eur. J. Biochem. 176,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig kappa chain precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 21-Jan-2000
A; Molecule type: mRNA
A; Residues: 1-219 <KWA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-234 <DE1>
                                                                                                                                                                  C; Accession: PC4203
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGSGSGTSYSLTISSVEAEDAATYYCQQY-SGYRTFGGGTKLEIKRADAAPTVSIFPPSS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EQLTSGGASVVCFLNNFYPRDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSMSSTLTLT 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MTQSPASLSVSVGESVTITCRASENIYSN-LAWYQQKQGKSPQLLVYVATKLVDGVPSRF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGSGSGTQYSLKINSLQSEDFGSYYCQHFWDTPFTFGSGTKLEMKRADAAPTVSIFPPSS 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 V.; van de Voorde, A.; Molemans, F.; Fiers, 287-295, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77.5%; Score 869; DB 2; 78.3%; Pred. No. 7.4e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19; Mismatches
                                                                                                                                                                                                                                                                                                                                                        234
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                                                                                                                                          S.H.; Park, Y.B.; Han,
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Ig kappa chain V region (clone 23.2) - C;Species: Mus musculus (house mouse) C;Date: 19-Oct-1995 #sequence_revision
                                          RESULT
A56169
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                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: mRNA
A;Residues: 1-219 <VAN>
A;Residues: 1-219 <VAN>
A;Cross-references: EMBL:L35138; NID:g522336; PIDN:AAA67525.1;
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology <IMM>
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A; Accession: S52028
A; Status: preliminary
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Best Local Similarity
Matches 168; Conser
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                                                                                                                                                                                                                        VPARFSGSGSGTSYSLTISSVEAEDAATYYCQQYSGY-RTFGGGTKLEIKRADAAPTVSI 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VLTQSPAIMSASPGEKVTMTCRASSSV----SSSYLHWYRQKSGASPKLWIYSTSNLASG 58
                                                                                                                                                                  FPPSSEQLTSGGASVVCFLNNFYPRDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSMSS 177
                                                                                                                                                                                                                                                             VMTQSPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFSG
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                                                                                                                                                                                                          VPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPPTFGGGTNLEIKRADAAPTVSI 122
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77.48;
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77.48;
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                                                                                                                                                                                                                                                                                                                 Score 861.5;
Pred. No. 2e-4
14; Mismatches
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Pred.
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    19-Oct-1995
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No. 2e-47;
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No. 8.6e-48;
                             (fragment)
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Ly mappa chain (Mab03-1) - mouse (fragic). Species: Mus musculus (house mouse) C;Date: 29-Jul-1997 #sequence_revision C;Accession: S68212
                                                                                                                                                                                                                                                                                                                                   R:Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; FEBS Lett. 375, 273-276, 1995
A:Title: Thermostable peroxidase activity with a recombinant antibody L chair A; Reference number: S68211; MUID:96085223
A; Accession: S68212
A; Status: preliminary; nucleic acid sequence not shown A; Molecule type: mRNA
A; Residues: 1-214 < TAK>
A; Cross-references: EMBL:D29668
C; Superfamily: immunoglobulin V region; immunoglobulin homology
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R;Monfardini, C.; Kieber-Emmons, T.; VonFeldt, J.M.; O'Malley, I J. Biol. Chem. 270, 6628-6638, 1995
A;Title: Recombinant antibodies in bioactive peptide design. A;Reference number: A56169; MUID:95204454
A;Accession: A56169
A;Status: preliminary; not compared with conceptual translation A;Status: preliminary; not compared with conceptual translation A;Molecule type: mRNA A;Residues: 1-210 <MON>
C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
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Best Local
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les 166; Conser
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STLTLTKDEYERHNSYTCEATHKTSTSPIVKS
                                                            LTLTKDEYERHNSYTCEATHKTSTSPIV
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                                                                                                                                                                                                                        VLTQSPAIMSASPGEKVTMTCRASSSVSSS-----YLHWYRQKSGASPKLWIYSTSNLAS
                                                                                                                                                                                            VMTQSPSSLAMSVGQKVTMSCKSSQSLLNSRNQKNYLAWYQQKPGQSPKLLVYFASTRES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VLTQSPASLTVSLGQRATISCRASKSVSSSGYSYMHWYQQKPGQPPKVLTYLASNLESGV
                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                       76.0%;
78.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mouse (fragment)
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                                                                                                                                                                                                                                                                          Pred. No.
                                                                                                                                                                                                                                                                                        Score
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                                                                                                                                                                                                                                                                         852; DB 2;
No. 7.9e-47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   recombinant antibody L chain-porphyr
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A; Experimental source: strain BALB/c, cell line RP93 hybridoma cell
A; Note: the authors translated the codon CGG for residue 106 as Pro, ACC for residue 132
A; Note: the nucleotide sequence shown is inconsistent with authors' translation because ect except for four positions shown above
C; Comment: The protein is an anti-phosphorylcholine antibody.
C; Superfamily: immunoglobulin v region; immunoglobulin homology
C; Keywords: immunoglobulin
    В
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                                                                                                                                                                                      C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;16-95/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                               R; Vaesen, M.; Frosch, M.; Weisgerber, C.; Eckart, K
Biol. Chem. Hoppe-Seyler 372, 451-453, 1991
A; Title: Primary structure of the murine monoclonal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             В
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F;7-106/Domain: V region #status predicted <VAR>
F;107-119/Domain: J region #status predicted <JIR>
F;120-225/Domain: C region #status predicted <COR>
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                                                                                                                                                                                                                                                           A; Molecule type: protein A; Residues: 1-219 <BIT>
                                                                                                                                                                                                                                                                                                                       A; Reference number: S16112; MUID: 92000313
A; Accession: S16112
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A; Residues: 1-225 <CHI>
                                                                                                                                                                                                                                                                                                                                                                                                                             Accession: S16112
                                                                                                                                                                                                                                                                                                                                                                                                                                                 g kappa chain V region (G2a) - mouse; Species: Mus musculus (house mouse); Date: 21-Nov-1993 #sequence_revision
                                                                                                        Query Match
Best Local
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                        VLTQSPAIMSASPGEKVTMTCRASSSV----SSSYLHWYRQKSGASPKLWIYSTSNLASG 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FPPSSEQLTSGGASVVCFLNNFYPRDINVKWKIDGSERONGVLNSWIDQDSKDSTYSMSS 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VPDRFSGSGSGTDFSLEISRVEAEDLGVYYCFQSSHVRWTFGGGTKLEIKRADAAPTVSI
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VMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLYWYLQKPGQSPKPLIYRVSNRFSG 62
                                                                                    Similarity 75.7
65; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76.0%;
76.5%;
                                                                                                        75.5%; Score 846.5; DB 2
75.7%; Pred. No. 1.8e-46;
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Pred. No. 8.9e-47;
                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                            Eckart, K.; Kratzin, H.; Bitter-Suermann,
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Search completed: Job time: 164 sec

June 18,

2001,

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A;Molecule type: mRNA
A;Residues: 1-217 <SCH>
A;Residues: 1-217 <SCH>
A;Cross-references: EMBL:X75536; NID:g414143; PIDN:CAA53226.1; PID:g414144
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
F;14-93/Domain: immunoglobulin homology <IMM>
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submitted to the EMBL Data Library, November 1993
A:Reference number: S42771
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C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S42772
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S42772
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                                    177
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                                                                                                                                                                                                                                                                         3 VLTQSPAIMSASPGEKVTMTCRASSSV----SSSYLHWYRQKSGASPKLWIYSTSNLASG 58
                                                                         IFPPSSEQLTSGGASVVCFLNNFYPRDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSMS 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . VPARFSGSGSGTSYSLTISSVEAEDAATYYCQQ--YSGYRTFGGGTKLEIKRADAAPTVS
                STITITKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 214
                                                                                                                                                                               VPARFSGSGSGTSYSLTISSVEAEDAATYYCQQYSGY--RTFGGGTKLEIKRADAAPTVS 116
                                                                                                                                                                                                                                    VMTQSPLSLPVSLGDQASISCRSSQSLVHTNGNTYLHWYLQKPGQSPKVLIYKVSTRFSG
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STLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRGEC
                                                                                                                                                       VPDRFSGSGSGTDFTFKISRVEAEDLGVYFCSQ-STYVPFTFGSGTKLEIKRADAAPTVS 119
                                                                                                                                                                                                                                                                                                                  al Similarity
165; Conserv
                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                75.48;
75.78;
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